

(TM)

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protein - protein database search, using Smith-Waterman algorithm

Tue Jan 18 09:51:49 2000; MasPar time 12.35 Seconds

not generated.

>US-09-332-063-2

4416

1 MPRAQPSASYQVPADPEA.....KTPIQILGQEPDAEMVEYLI 675

PAM 150

## Gap 11

130303 seqs, 12848679 residues

Minimum Match 08

a-issued

1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1

Mean 34.900; Variance 263.923; scale 0.132

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result	?	Score	Query Match	Length	DB	ID	Description	Pred. No
1	284	6.4	214	1	US-08-217-	Sequence 4, Applicatio	2.53e-07	
2	259	5.9	180	4	5273901-7	Patent No. 5273901.	4.99e-07	
3	259	5.9	180	4	5482709-6	Patent No. 5482709.	4.99e-07	
4	257	5.8	186	1	US-08-450-	Sequence 2, Applicatio	6.32e-07	
5	246	5.6	219	2	US-08-557-	Sequence 54, Applicati	2.32e-07	
6	245	5.5	234	1	US-08-642-	Sequence 51, Applicati	2.61e-07	
7	245	5.5	561	1	US-08-642-	Sequence 52, Applicati	2.61e-07	
8	243	5.5	907	3	PCR-US95-0	Sequence 19, Applicati	3.31e-07	
9	241	5.5	2441	1	US-08-194-	Sequence 2, Applicatio	4.19e-07	
10	238	5.4	262	2	US-08-929-	Sequence 1, Applicatio	5.96e-07	
11	238	5.4	262	2	US-08-403-	Sequence 1, Applicatio	5.96e-07	
12	238	5.4	263	2	US-08-557-	Sequence 51, Applicati	5.96e-07	
13	240	5.4	297	2	US-08-580-	Sequence 6, Applicatio	4.71e-07	
14	238	5.4	447	1	US-08-450-	Sequence 4, Applicatio	5.95e-07	
15	234	5.3	330	1	US-08-642-	Sequence 32, Applicati	9.54e-07	
16	224	5.2	408	1	US-07-609-	Sequence 65, Applicati	1.93e-07	
17	228	5.2	1248	2	US-09-080-	Sequence 2, Applicatio	2.43e-07	
18	226	5.1	98	2	US-07-812-	Sequence 2, Applicatio	2.43e-07	
19	226	5.1	98	2	US-07-814-	Sequence 2, Applicatio	2.16e-07	
20	227	5.1	777	1	US-08-642-	Sequence 53, Applicati	4.90e-07	
21	220	5.0	2035	2	US-08-479-	Sequence 2, Applicatio	8.76e-07	
22	215	4.9	475	2	US-08-396-	Sequence 14, Applicati	8.76e-07	
23	215	4.9	475	2	US-08-861-	Sequence 14, Applicati	8.76e-07	

25	2.5	2.16	4.9	7.22	4	5200183-3	Patient No. 5200183.	7.80e-04
24	2.5	2.16	4.9	7.22	1	US-08-204-	Sequence 7, Applicatio	7.80e-04
23	2.6	2.16	4.9	7.22	1	US-08-347-	Sequence 1, Applicatio	7.80e-04
22	2.6	2.16	4.9	7.22	1	US-08-442-	Sequence 1, Applicatio	7.80e-04
21	2.6	2.16	4.9	7.22	1	US-08-445-	Sequence 3, Applicatio	7.80e-04
20	2.9	2.16	4.9	7.22	1	US-08-445-	Sequence 3, Applicatio	7.80e-04
19	3.0	2.16	4.9	7.22	1	US-08-445-	Sequence 3, Applicatio	7.80e-04
18	3.1	2.16	4.9	7.22	1	5200183-2	Patient No. 5200183.	7.80e-04
17	3.2	2.16	4.9	7.42	1	US-08-347-	Sequence 2, Applicatio	7.80e-04
16	3.3	2.16	4.9	7.42	2	US-08-442-	Sequence 2, Applicatio	7.80e-04
15	3.4	2.16	4.9	7.45	1	US-08-445-	Sequence 2, Applicatio	7.80e-04
14	3.5	2.16	4.9	7.45	2	US-08-204-	Sequence 2, Applicatio	7.80e-04
13	3.6	2.17	4.9	10.26	1	US-08-614-	Sequence 7, Applicatio	6.94e-04
12	3.7	2.13	4.8	10.26	2	US-08-614-	Sequence 7, Applicatio	6.94e-04
11	3.8	2.11	4.8	10.77	1	US-07-972-	Sequence 82, Applicati	1.10e-03
10	3.9	2.11	4.8	10.77	1	US-08-442-	Sequence 95, Applicati	1.39e-03
9	4.0	2.14	4.8	18.67	2	US-08-642-	Sequence 5, Applicatio	9.83e-04
8	4.2	2.09	4.7	24.14	1	US-08-227-	Sequence 2, Applicatio	1.75e-03
7	4.2	2.09	4.7	24.14	3	PCT-US95-1	Sequence 2, Applicatio	1.75e-03
6	4.3	2.05	4.6	12.55	2	US-09-080-	Sequence 4, Applicatio	2.78e-03
5	4.4	1.97	4.5	7.23	4	5200183-4	Patient No. 5200183.	6.96e-03
4	4.5	1.95	4.4	14.4	1	US-08-642-	Sequence 49, Applicati	8.78e-03

## ALIGNMENTS

RESULT	1	STANDARD	PRT	214 AA.
ID	US-08-217-327-4			
XX				
AC	xxxxxx			
DT				
XX				
DE	Sequence 4, Application US/08217327			
XX				
CC	Sequence 4, Application US/08217327			
CC	Patent No. 5474925			
CC	GENERAL INFORMATION:			
CC	APPLICANT: John, Maliyakal E			
CC	APPLICANT: Barton, Kenneth A			
CC	TITLE OF INVENTION: Immobilized Proteins in Cotton Fiber			
CC	NUMBER OF SEQUENCES: 16			
CC	CORRESPONDENCE ADDRESS:			
CC	ADDRESSEE: Quarles and Brady			
CC	STREET: P.O. Box 2113			
CC	CITY: Madison			
CC	STATE: WI			
CC	COUNTRY: USA			
CC	ZIP: 53701-2113			
CC	COMPUTER READABLE FORM:			
CC	MEDIUM TYPE: Floppy disk			
CC	COMPUTER: IBM PC compatible			
CC	OPERATING SYSTEM: PC-DOS/MS-DOS			
CC	SOFTWARE: PatentIn Release #1.0, Version #1.25			
CC	CURRENT APPLICATION DATA:			
CC	APPLICATION NUMBER: US/08/217,327			
CC	FILING DATE:			
CC	CLASSIFICATION: 435			
CC	PRIOR APPLICATION DATA:			
CC	APPLICATION NUMBER: US 07/812,233			
CC	FILING DATE: 19-DEC-1991			
CC	ATTORNEY/AGENT INFORMATION:			
CC	NAME: Seay, Nicholas J			
CC	REGISTRATION NUMBER: 27,386			
CC	REFERENCE/DOCKET NUMBER: 1122990831			
CC	TELECOMMUNICATION INFORMATION:			
CC	TELEPHONE: 608-251-5000			
CC	TELEFAX: 608-251-9166			
CC	INFORMATION FOR SEQ ID NO: 4:			
CC	SEQUENCE CHARACTERISTICS:			
CC	LENGTH: 214 amino acids			
CC	TYPE: amino acid			
CC	TOPOLOGY: linear			

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CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: Patentm Release #1.0, Version #1.30 (EPO
CC      CURRENT APPLICATION DATA:
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CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: MAKI, David J.
CC REGISTRATION NUMBER: 31,392
CC REFERENCE/DOCKET NUMBER: 210121.422
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206) 622-4900
CC TELEFAX: (206) 682-6031
CC INFORMATION FOR SEQ ID NO: 54:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 219 amino acids
CC TYPE: amino acid
CC STRANDEDNESS:
CC TOPOLOGY: linear
CC SEQ SEQUENCE 219 AA; 21347 MW; 161993 CN;

Query Match 5.6%; Score 246; DB 2; Length 219;
Best Local Similarity 37.9%; Pred. No. 2.32e-05;
Matches 59; Conservative 43; Mismatches 52; Indels 0; Gaps

Db 56 AAAAAAOKAAAKKAAAPSGKSKSAAPAKAAAPAKAAAPAKAAAPAKAAAHAKA 115
QY 476 APVAAAAATAATITTTVAAPVAVAAAAAPAAAAAPSPATNAATAAVSRAA 535
Dd 116 AAPAKAAPAKPRAKPRAKPRAKPRAKPRAKPRAKPRAKPRAKPRAKPRAKPRAK 175
QY 536 GOIPAAASVAAAVAPSPAAAAVQVAPAPAPAPAPAPAPAPAPAPAPAAQASAPAQAP 595
Db 176 AKAAPPAKAAAPPAKAAAPPAKAAAPPAKAAAPPAKAAAPPAKAAAPPAKAAAP 208
QY 596 TSAAPAVAPPTPTPTPAVAAQEVAPASPTATGCP 628

RESULT 6 STANDARD; PRT: 234 AA.
XX ID US-08-642-255-51
AC xxxxxx
DT
DE
XX Sequence 51, Application US/08642255
CC
CC Sequence 51, Application US/08642255
CC Patent No. 5773249
CC GENERAL INFORMATION:
CC APPLICANT: CAPPELLO, Joseph
CC APPLICANT: FERRARI, Franco A.
CC TITLE OF INVENTION: High Molecular Weight Collagen-Like
CC TITLE OF INVENTION: Protein Polymers
CC NUMBER OF SEQUENCES: 135
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
CC STEER: 4 Embarcadero Center, Suite 3400
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94111-4187
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/642,255
CC FILING DATE:
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: ROWLAND, Berttram I.
CC REGISTRATION NUMBER: 20,015
CC REFERENCE/DOCKET NUMBER: A55556-3/BIR
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 494-8700
CC TELEFAX: (415) 494-8701

```



CC LENGTH: 907 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
SQ SEQUENCE 907 AA; 94489 MW; 5007079 CN;

Query Match 5.5%; Score 243; DB 3; Length 907;  
Best Local Similarity 22.5%; Pred. No. 3.31e-05;  
Matches 50; Conservative 86; Mismatches 80; Indels 6; Gaps 6;

Db 471 ADVTSPTAGTSGASPTSPSPMDNGE-SKAPDMSSTSPVTPPTPNATSPPTAVTT 529  
OY 429 PSTSPVPTPLSHSKSGSDCSTQTERGTEENKTAAPVAVPAAAAATAAAT 488  
Db 530 PTPNATSPPTAVTTPP-NATSPITGKTSPTSAVTPPTPNATSPPL-CKTSPSTAVTPT 587  
OY 489 ATAATTTTMAAAVAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 548  
Db 588 PNATSPITGKTSPTSAVTPPTPNAT-GPTVGETSPQANATNHTIGTSPPTVVTGPKN 645  
OY 549 AVAASAAAAAAVAP 608  
Db 646 ATSAVTTGQHNITSSSTSMISRPSSNETLSPSTSDNSTH 687  
OY 609 PTPAQAQEV-ASPATGPGPHRLSIPILCNPKTDGPFVH 649

RESULT 9  
ID US-08-194-468-2 STANDARD: PRT; 2441 AA.  
XX xxxxxx

Sequence 2, Application US/08194468  
Patent No. 5750336  
GENERAL INFORMATION:  
APPLICANT: Montmady, Marc R.  
TITLE OF INVENTION: ASSAYS FOR THE IDENTIFICATION OF  
TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT ACTIVATION OF CAMP AND MITOGEN  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/194,468  
FILING DATE: 10-FEB-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P41 9672  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)-546-4737  
TELEFAX: (619)-546-9392  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2441 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

SQ SEQUENCE 2441 AA; 265473 MW; 30223014 CN;

Query Match 5.5%; Score 241; DB 1; Length 2441;  
Best Local Similarity 23.4%; Pred. No. 4.19e-05;  
Matches 58; Conservative 89; Mismatches 91; Indels 10; Gaps 10;

Db 764 SPSPPOPPNMGTHANNIMQAPNQNFPLPQNGEPSSSGAMSVNMGCPAAGVSO 823  
OY 431 TPSEVPSTPLSHSKSGSDCSTQTERGTEENKTAAPVAVPAAAAATAAATA 489  
Db 824 GOERGAALPNLMLAPQSLPCPVYQSPPLHPTPPASTAGMPSLQHTAPGMTBPQ 883  
OY 490 TAATTTTMAAAVAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 548  
Db 884 PAAPQSTPVSSQOTPTPTGVSVAQAQSTPTVQAQAQVTPPOPPTVPPSVATP 943  
OY 549 AVAS-AAA-AAVQVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 603  
Db 944 QSSQOQPTPVHTQPGPPLSQAASIDNVPTPSTVSAETSSQCPGPDVPLEKTEVQ 1003  
OY 604 -TPAPTPPAAQA-EVPASPTGPGPHRLSIPS-LICNPDKTDGPFVHSLERKPIQ 660  
Db 1004 TDDAEPP 1011  
OY 661 ILGGEPPA 668

RESULT 10  
ID US-08-929-414-1 STANDARD: PRT; 262 AA.  
XX xxxxxx

Sequence 1, Application US/08929414  
Patent No. 5942403  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Houghton, Raymond  
TITLE OF INVENTION: OF T. CRUZI INFECTION  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/929,414  
FILING DATE: 15-SEP-1997  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 210121.406C1  
REFERENCE/DOCKET NUMBER: 210121.406C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 262 amino acids  
TYPE: amino acid  
TOPOLOGY: linear





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XX      xx      xxxxxx
AC
XX      XX
DT
XX      XX
DE
XX      XX
Sequence 32, Application US/08642255
CC      CC      Sequence 32, Application US/08642255
CC      CC      Patent No. 5773249
CC      CC      GENERAL INFORMATION:
CC      CC      APPLICANT: CARPANELLO, Joseph
CC      CC      APPLICANT: FERRARI, Franco A.
CC      CC      TITLE OF INVENTION: High Molecular Weight Collagen-Like
CC      CC      TITLE OF INVENTION: Protein Polymers
CC      CC      NUMBER OF SEQUENCES: 135
CC      CC      CORRESPONDENCE ADDRESS:
CC      CC      ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
CC      CC      STREET: 4 Embarcadero Center, Suite 3400
CC      CC      CITY: San Francisco
CC      CC      STATE: California
CC      CC      COUNTRY: USA
CC      CC      ZIP: 94111-4187
CC      CC      COMPUTER READABLE FORM:
CC      CC      MEDIUM TYPE: Floppy disk
CC      CC      COMPUTER: IBM PC compatible
CC      CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      CC      SOFTWARE: Patentin Release #1.0, Version #1.30
CC      CC      CURRENT APPLICATION DATA:
CC      CC      APPLICATION NUMBER: US/08/642,255
CC      CC      FILING DATE:
CC      CC      CLASSIFICATION: 435
CC      CC      ATTORNEY/AGENT INFORMATION:
CC      CC      NAME: ROWLAND, Bertram I.
CC      CC      REGISTRATION NUMBER: 20,015
CC      CC      REFERENCE/DOCKET NUMBER: A55556-3/BIR
CC      CC      TELECOMMUNICATION INFORMATION:
CC      CC      TELEPHONE: (415) 494-8700
CC      CC      TELEFAX: (415) 494-8771
CC      CC      TELEX: 910 277299 EHT UR
CC      CC      INFORMATION FOR SEQ ID NO: 32:
CC      CC      SEQUENCE CHARACTERISTICS:
CC      CC      LENGTH: 330 amino acids
CC      CC      type: amino acid
CC      CC      STRANDEDNESS: single
CC      CC      TOPOLOGY: linear
CC      CC      MOLECULE TYPE: protein
CC      CC      SEQUENCE 330 AA; 28876 MW; 625100 CN;
SO
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st Local Similarity 22.1%; Pred. No. 9,54e-05;
Matches 49; Conservative 90; Mismatches 76; Indels 7; Gaps 7;
Db 36 PGPDPGPPGPGAGCPGCGPPGGPGGPGAGPVGSFGAGCPGPGPGPGAGAPGPPG 95
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OY 429 PSTSP-PPSTP-LLSHSKTSGRDCSTOTERGETSENKTAVAIVPAVAAATAA 486
   | : : | : : | : : : | : : : | : : : | : : : | : : : | : : :
Db 96 PGPPGPPGPPGVCS-GCAPGPPGPPGPPGPGAGAGPPGPPGPPGPPGPPGAGC 154
   | : : | : : | : : : | : : : | : : : | : : : | : : : | : : :
OY 487 ITATRAATTITMVAALPYAVAAAAAP-SPATRAATAAVSFAAAGQIPAAASVA 545
   | : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db 155 PGPDPGPPGADGPPGPPGPPGPA-GPVGSPGAPGPPGPPGPPGAPG-PGPP 212
   | : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
OY 546 SAAVAAPSAALAAVAVAPAAPVAPVALVPVAPAPAQAASNAQIQTATSNVAPT 605
   | : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db 213 PGPPGPPGPPGAGCPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPP 254
   | : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
OY 606 APTTPAAQAEVPAASPATGP-GHRLISTLTCTCNPDXTDGP 646

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Search completed: Tue Jan 18 09:52:05 2000  
Job time : 16 secs.





	Query Match	8.1%;	Score 359;	DB 5;	Length 807;	
	Best Local Similarity	34.2%;	Pred.	No.1.12e-14;		
	Matches	67;	Conservative	69;	Mismatches 51;	Indels 9; Gaps 9;
Dd	521	PTAAAPVPTTAAI-PAPATAAPT-AAPTTAESPVTYTVPTAAPTAAPTAVEIP	578			
Oy	429	PSPPSPVPSTPLSHSKTSGSDCTOTERGESKNTAAVAISVPAPAAAAATAA-AI	487			
Dd	579	IYTSAPTAAPAPTAAPAPTAVPEIPTVTSPTAAPTAAAPANTTVTPPTAP	638			
Oy	488	TATAA-TITTTMW-AAAPVAIAAAAAPA-AAAPSPATAATAAVASPAAGCIPAAASV	544			
Dd	639	TTAAP-AAPIYTATPPTAAPTAAAPANT-VTVEPTAAPTAAPIVADPNTTAAPVTT	696			
Oy	545	ASAAAAPSAAAAAAAAQVAPAAPAPAPALVPAPAPAAOASAPAQOTAF-TSAPAVAP	603			
Dd	697	TSAPATPEDDDIDDP	712			
Oy	604	TPAPPTPAPVAQAEVP	619			
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ID	039782	PRELIMINARY:	PRT;	867	AA.	
AC	039782:					
DT	01-JAN-1998	(TREMBREL. 05, CREATED)				
DT	01-JAN-1998	(TREMBREL. 05, LAST SEQUENCE UPDATE)				
DE	01-JAN-1998	(TREMBREL. 05, LAST ANNOTATION UPDATE)				
DE	MEMBRANE GLYCOPROTEIN.					
OS	EQUINE HERPESVIRUS 1.					
OC	VIRUSES; DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE;					
CC	ALPHAHERPESVIRINAE; VARICELLOVIRUS.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN-BK343;					
RA	KIRISAWA R., KOBAYASHI T., KAMAKAMI Y., IMAI H.;					
RL	J. EQUINE SCI. 7:79-87(1996).					
DR	EMB.; D88734; D1020846; --					
KW	MEMBRANE.					
SO	SEQUENCE	867 AA;	86630 MW;	DC3E8AA2	CRC32;	
	Query Match	7.7%;	Score 341;	DB 14;	Length 867;	
	Best Local Similarity	26.3%;	Pred.	No.2.47e-13;		
	Matches	57;	Conservative	91;	Mismatches 67;	Indels 2; Gaps 2;
Dd	168	TTATTVPPTASTDPTDTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA	227			
Oy	430	STPSVVPSTPLSHSKTSGHDSCTOTERGESKNTAAVAISVPAPAAAAATTAATA	489			
Dd	228	AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	287			
Oy	490	TAAITTTTMMVAAPVAIAAAAAPAAAAAPSPATAATTAASPAAGAQPAAASVASMAA	549			
Dd	288	TTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	347			
Oy	550	VAPSAASAAAAQVAPAAPAPAPALVPAPAPAAOASAPAQOTAFPSAPAVAP-TPAPT	608			
Dd	348	PSASTATSATPTSISTASAAT-STPTPTSATSAES	383			
Oy	609	PTPAPVAQAEVPASPATGCPHRSLIPSLTCNDPKTKD	645			
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AC	P91365:					
DT	01-MAY-1997	(TREMBREL. 03, CREATED)				
DT	01-MAY-1997	(TREMBREL. 03, LAST SEQUENCE UPDATE)				
DT	01-NOV-1998	(TREMBREL. 08, LAST ANNOTATION UPDATE)				
DE	CODED FOR BY C. ELEGANS CDNA YK50C7.5.					
GN	K06A9.1.					
OS	CAENORHABDITIS ELEGANS.					
CC	HABEROTA; METAPOA; NEMATODA; SEGERMENTEA; RHABDITIA; RHABDITIDA;					
CC	RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.					
NC	[1]					

SQ	SEQUENCE	788 AA;	81716 MW;	9F8ADE83 CRC32;
	Query Match	7.6%;	Score 335;	DB 5; Length 788;
	Best Local Similarity	28.6%;	Pred. No. 6,88e-13;	
	Matches	55; Conservative	77; Mismatches	58; Indels 2; Gaps 2
Dd	PTAAPSTPVPPEPPATAAPVPPPTAAPTAAAPTAAPTAAPTAAPTAAPTTATTP	562		
Oy	PSIPSPVPSPPLLSAHSKTGSRCDSOTERGETSNTKAAPISVPAPVAAAATAIT	488		
Dd	563 AAPTAAPTAVPELPDIYTSAPTAAPTAAPTAAPTAAPTAAPTAAPTVAPEIPTVSPTPAAPTA	622		
Oy	ATAATTITTMTWAAAPVAAAAAAPPAAASPATAATAAVSPAQAQQIPAASVASAA	548		
Dd	623 AAPATTVTVPPLAAPTAAAPAPMPT -TVTPPTAAPTAAPTAAPTVAHPPTTAAPVTTTSAP	681		
Oy	AAPSAAPAAAAVOYAPAAPAPVAPALVPVAPAPAAQASAPAQTOP -TSAPAPVAPAP	607		
Dd	682 ATPEDDIDDEP 693			
Oy	TPPRAVNAQAEVP 619			
RESULT	7 PRELIMINARY; PRT; 866 AA.			
ID	039781			
AC	039781;			
DT	01-JAN-1998 (TREMBLEL. 05, CREATED)			
DT	01-JAN-1998 (TREMBLEL. 05, LAST SEQUENCE UPDATE)			
DT	01-JAN-1998 (TREMBLEL. 05, LAST ANNOTATION UPDATE)			
OS	MEMBRANE GLYCOPROTEIN.			
OC	EQUINE HERPESVIRUS 1.			
CC	VIRUSES; DSDNA VIRUSES; NO RNA STAGE; HERPESVIRIDAE;			
CC	ALPHAHERPESVIRINAE; VARICELLOVIRUS.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-HH1;			
RA	KIRISAWA R., KOBAYASHI T., KAMAKAMI Y., IWAI H.;			
RL	J. EQUINE SCI. 7:79-87(1996).			
RM	EMBL; D88733; D1020845; .			
KX	MEMBRANE.			
SQ	SEQUENCE 866 AA; 86463 MW; 7200333A CRC32;			
	Query Match	7.6%;	Score 335;	DB 14; Length 866;
	Best Local Similarity	25.2%;	Pred. No. 6.88e-13;	
	Matches	55; Conservative	90; Mismatches	71; Indels 2; Gaps 2
Dd	166 PTSTTTTTATTVTPTASTTTDDTTAATTAATTAATTAATTAATTAATTAATTAATTT	225		
Oy	429 PSTSPVPSPSTPLLSAHSKTGSRCDSOTERGETSNTKAAPISVPAPVAAAATAIT	488		
Dd	226 AATTAAATTAATTAATTAATTSATTAATTAATTAATTAATTAATTAATTAATTAATTA	285		
Oy	489 ATAATTITTMTWAAAPVAAAAAAPPAAASPATAATAAVSPAQAQQIPAASVASAA	548		
Dd	286 ATTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTGSSGSTTGCASTS	345		
Oy	549 AVAASAAPAAAAVOYAPAAPAPVAPALVPVAPAPAAQASAPAQTOPATSAPAVAP -TPAP	607		
Dd	346 TPSASTATSAPTSTSTAATT -STPTPSAATSAES 382			
Oy	608 TPPRAVNAQAEVPAPATGPGPHRLSTPLSLCNPDXTKG 645			
RESULT	8 PRELIMINARY; PRT; 801 AA.			
ID	023635			
AC	023635;			
DT	01-NOV-1996 (TREMBLEL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLEL. 01, LAST SEQUENCE UPDATE)			
DT	01-NOV-1998 (TREMBLEL. 08, LAST ANNOTATION UPDATE)			
DE	IDENTICAL TO LONG TANDEM REPEAT REGION OF SIALIDASE.			
GN	ZK84.1.			
CS	CANDORHADITIS ELEGRANS.			
CC	ERAPORCIB - METZGAU NDUNACOD - CCGEDRUTTC - SWITZERLAND - TWISTE			



RP  
RC SEQUENCE FROM N.A.  
RD STRAIN-NS80567;  
RE MEDLINE: 98264497.  
RF TELFORD E.A.R., WATSON M.S., PERRY J., CULLINANE A.A., DAVIDSON A.J.  
RG "The DNA sequence of equine herpesvirus-4.";  
RH J. GEN. VIROL. 79:1197-1203(1998).  
RI [4]  
RJ SEQUENCE FROM N.A.  
RK

[illegible]



...DEARN...SVKG--LIQVEDGK 2610

RESULT 4  
US-08-403-379A-1  
; Sequence 1, Application US/08403379A  
; Patent No. 5756662  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION  
; TITLE OF INVENTION: OF T. CRUZI INFECTION  
; NUMBER OF SEQUENCES: 9

32-06:

3

CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,379A  
FILING DATE: 14-MAR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.406  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 262 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-403-379A-1

Query Match 6.4%; Score 213; DB 1; Length 262;  
Best Local Similarity 48.4%; Pred. No. 2.8e-07;  
Matches 74; Conservative 9; Mismatches 54; Indels 16; Gaps 9;  
QY 479 AAAATAAAITATA.TITTTMVAAP---VAVAAAAAPA-AAAAPSPATAAAATAAVSPAA 534  
Db 112 AAAAAAAKQKAAAK-----AAAPSGKKSAKAAIAPAKAAAAAPAKAAAAAPAK 165  
QY 535 AGQIPAAASVASA-AAVAPSAAAAAVQVAPAPVPAPALVPVPAPAAAQASAPAQTO 593  
Db 166 AAAAPAKAAAAAPAKAATAPAKAAAAAPAKTA-AAAPAKAAAPAKA-AAAPAKA-ATAPAKAA 222  
QY 594 AFTSAPAVAPTPTPTTPAVAQAEVPASPATGP 626  
Db 223 AAPAKAATAPAKAAT-APAKA-AAAPAKAATAP 253

RESULT 5